

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Amara, Susan G
Arriza, Jeffrey L

(ii) TITLE OF INVENTION: Amino Acid Transporters and Uses

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Allegretti & Witcoff, Ltd.
(B) STREET: 10 South Wacker Drive, Suite 3000
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 93,509

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-715-1000
(B) TELEFAX: 312-715-1234
(C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Amara, Susan G
Arriza, Jeffrey L
- (ii) TITLE OF INVENTION: Amino Acid Transporters and Uses
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Allegretti & Witcoff, Ltd.
 - (B) STREET: 10 South Wacker Drive, Suite 3000
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/140,729
 - (B) FILING DATE: 20 OCT 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Noonan, Kevin E
 - (B) REGISTRATION NUMBER: 35,303
 - (C) REFERENCE/DOCKET NUMBER: 93,509
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-715-1000
 - (B) TELEFAX: 312-715-1234
 - (C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGRGCRATG AARATGGCAG CCAGGGCYTC ATACAGGGCT GTGCCRTCCA TGTTRATGGT

60

RGC

63

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: 5'UTR
(B) LOCATION: 1..30

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 31..1626

(ix) FEATURE:
(A) NAME/KEY: 3'UTR
(B) LOCATION: 1626..1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACCTCTAGC TCGGAGCGGC GTGTAGCGCC ATG GAG AAG AGC AAC GAG ACC AAC	54
Met Glu Lys Ser Asn Glu Thr Asn	
1 5	
GGC TAC CTT GAC AGC GCT CAG GCG GGG CCT GCG GCC GGG CCC GGA GCT	102
Gly Tyr Leu Asp Ser Ala Gln Ala Gly Pro Ala Ala Gly Pro Gly Ala	
10 15 20	
CCG GGG ACC GCG GCG GGA CGC GCA CGG CGT TGC GCG CGC TTC CTG CGG	150
Pro Gly Thr Ala Ala Gly Arg Ala Arg Arg Cys Ala Arg Phe Leu Arg	
25 30 35 40	
CGC CAA GCG CTG GTG CTG CTC ACC GTG TCC GGG GTG CTG GCG GGC GCG	198
Arg Gln Ala Leu Val Leu Leu Thr Val Ser Gly Val Leu Ala Gly Ala	
45 50 55	
GGC CTG GGC GCG GCG TTG CGC GGG CTC AGC CTG AGC CGC ACG CAG GTC	246
Gly Leu Gly Ala Ala Leu Arg Gly Leu Ser Leu Ser Arg Thr Gln Val	
60 65 70	
ACC TAC CTG GCC TTC CCC GGC GAG ATG CTG CTC CGC ATG CTG CGC ATG	294
Thr Tyr Leu Ala Phe Pro Gly Glu Met Leu Leu Arg Met Leu Arg Met	
75 80 85	
ATC ATC CTG CCG CTG GTG GTC TGC AGC CTG GTG TCG GGC GCC GCC TCG	342
Ile Ile Leu Pro Leu Val Val Cys Ser Leu Val Ser Gly Ala Ala Ser	
90 95 100	
CTC GAT GCC AGC TGC CTC GGG CGT CTG GGC GGC ATC CGT GTC GCC TAC	390
Leu Asp Ala Ser Cys Leu Gly Arg Leu Gly Gly Ile Arg Val Ala Tyr	
105 110 115 120	
TTT GGC CTC ACC ACA CTG AGT GCC TCG GCG CTC GCC GTG GCC TTG GCG	438
Phe Gly Leu Thr Thr Leu Ser Ala Ser Ala Leu Ala Val Ala Leu Ala	
125 130 135	

TTC ATC ATC AAG CCA GGA TCC GGT GCG CAG ACC CTT CAG TCC AGC GAC	486
Phé Ile Ile Lys Pro Gly Ser Gly Ala Gln Thr Leu Gln Ser Ser Asp	
140 145 150	
CTG GGG CTG GAG GAC TCG GGG CCT CCT CCT GTC CCC AAA GAG ACG GTG	534
Leu Gly Leu Glu Asp Ser Gly Pro Pro Pro Val Pro Lys Glu Thr Val	
155 160 165	
GAC TCT TTC CTC GAC CTG GCC AGA AAC CTG TTT CCC TCC AAT CTT GTG	582
Asp Ser Phe Leu Asp Leu Ala Arg Asn Leu Phe Pro Ser Asn Leu Val	
170 175 180	
GTT GCA GCT TTC CGT ACG TAT GCA ACC GAT TAT AAA GTC GTG ACC CAG	630
Val Ala Ala Phe Arg Thr Tyr Ala Thr Asp Tyr Lys Val Val Thr Gln	
185 190 195 200	
AAC AGC AGC TCT GGA AAT GTA ACC CAT GAA AAG ATC CCC ATA GGC ACT	678
Asn Ser Ser Ser Gly Asn Val Thr His Glu Lys Ile Pro Ile Gly Thr	
205 210 215	
GAG ATA GAA GGG ATG AAC ATT TTA GGA TTG GTC CTG TTT GCT CTG GTG	726
Glu Ile Glu Gly Met Asn Ile Leu Gly Leu Val Leu Phe Ala Leu Val	
220 225 230	
TTA GGA GTG GCC TTA AAG AAA CTA GGC TCC GAA GGA GAA GAC CTC ATC	774
Leu Gly Val Ala Leu Lys Lys Leu Gly Ser Glu Gly Glu Asp Leu Ile	
235 240 245	
CGT TTC TTC AAT TCC CTC AAC GAG GCG ACG ATG GTG CTG GTG TCC TGG	822
Arg Phe Phe Asn Ser Leu Asn Glu Ala Thr Met Val Leu Val Ser Trp	
250 255 260	
ATT ATG TGG TAC GTA CCT GTG GGC ATC ATG TTC CTT GTT GGA AGC AAG	870
Ile Met Trp Tyr Val Pro Val Gly Ile Met Phe Leu Val Gly Ser Lys	
265 270 275 280	
ATC GTG GAA ATG AAA GAC ATC ATC GTG CTG GTG ACC AGC CTG GGG AAA	918
Ile Val Glu Met Lys Asp Ile Ile Val Leu Val Thr Ser Leu Gly Lys	
285 290 295	
TAC ATC TTC GCA TCT ATA TTG GGC CAT GTT ATT CAT GGA GGA ATT GTT	966
Tyr Ile Phe Ala Ser Ile Leu Gly His Val Ile His Gly Gly Ile Val	
300 305 310	
CTG CCA CTT ATT TAT TTT GTT TTC ACA CGA AAA AAC CCA TTC AGA TTC	1014
Leu Pro Leu Ile Tyr Phe Val Phe Thr Arg Lys Asn Pro Phe Arg Phe	
315 320 325	
CTC CTG GGC CTC CTC GCC CCA TTT GCG ACA GCA TTT GCT ACC TGC TCC	1062
Leu Leu Gly Leu Leu Ala Pro Phe Ala Thr Ala Phe Ala Thr Cys Ser	
330 335 340	
AGC TCA GCG ACC CTT CCC TCT ATG ATG AAG TGC ATT GAA GAG AAC AAT	1110
Ser Ser Ala Thr Leu Pro Ser Met Met Lys Cys Ile Glu Glu Asn Asn	
345 350 355 360	
GGT GTG GAC AAG AGG ATC AGC AGG TTT ATT CTC CCC ATC GGG GCC ACC	1158
Gly Val Asp Lys Arg Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr	
365 370 375	

GTG AAC ATG GAC GGA GCA GCC ATC TTC CAG TGT GTG GCC GCG GTG TTC Val Asn Met Asp Gly Ala Ala Ile Phe Gln Cys Val Ala Ala Val Phe 380 385 390	1206
ATT GCG CAA CTC AAC AAC ATA GAG CTC AAC GCA GGA CAG ATT TTC ACC Ile Ala Gln Leu Asn Asn Ile Glu Leu Asn Ala Gly Gln Ile Phe Thr 395 400 405	1254
ATT CTA GTG ACT GCC ACA GCG TCC AGT GTT GGA GCA GCA GGC GTG CCA Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Val Pro 410 415 420	1302
GCT GGA GGG GTC CTC ACC ATT GCC ATT ATC CTG GAG GCC ATT GGG CTG Ala Gly Gly Val Leu Thr Ile Ala Ile Ile Leu Glu Ala Ile Gly Leu 425 430 435 440	1350
CCT ACT CAT GAC CTG CCT CTG ATC CTG GCT GTG GAC TGG ATT GTG GAC Pro Thr His Asp Leu Pro Leu Ile Leu Ala Val Asp Trp Ile Val Asp 445 450 455	1398
CGG ACC ACC ACG GTG GTG AAT GTG GAG GGG GAT GCC CTG GGT GCA GGC Arg Thr Thr Val Val Asn Val Glu Gly Asp Ala Leu Gly Ala Gly 460 465 470	1446
ATT CTC CAC CAC CTG AAT CAG AAG GCA ACA AAG AAA GGC GAG CAG GAA Ile Leu His His Leu Asn Gln Lys Ala Thr Lys Lys Gly Glu Gln Glu 475 480 485	1494
CTT GCT GAG GTG AAA GTG GAA GCC ATC CCC AAC TGC AAG TCT GAG GAG Leu Ala Glu Val Lys Val Glu Ala Ile Pro Asn Cys Lys Ser Glu Glu 490 495 500	1542
GAG ACA TCG CCC CTG GTG ACA CAC CAG AAC CCC GCT GGC CCC GTG GCC Glu Thr Ser Pro Leu Val Thr His Gln Asn Pro Ala Gly Pro Val Ala 505 510 515 520	1590
AGT GCC CCA GAA CTG GAA TCC AAG GAG TCG GTT CTG TGATGGGGCT Ser Ala Pro Glu Leu Glu Ser Lys Glu Ser Val Leu 525 530	1636
GGGCTTTGGG CTTGCCTGCC AGCAGTGATG TCCCCACCTG TTCA	1680

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Lys Ser Asn Glu Thr Asn Gly Tyr Leu Asp Ser Ala Gln Ala 1 5 10 15
Gly Pro Ala Ala Gly Pro Gly Ala Pro Gly Thr Ala Ala Gly Arg Ala 20 25 30

Arg Arg Cys Ala Arg Phe Leu Arg Arg Gln Ala Leu Val Leu Leu Thr
35 40 45

Val Ser Gly Val Leu Ala Gly Ala Gly Leu Gly Ala Ala Leu Arg Gly
50 55 60

Leu Ser Leu Ser Arg Thr Gln Val Thr Tyr Leu Ala Phe Pro Gly Glu
65 70 75 80

Met Leu Leu Arg Met Leu Arg Met Ile Ile Leu Pro Leu Val Val Cys
85 90 95

Ser Leu Val Ser Gly Ala Ala Ser Leu Asp Ala Ser Cys Leu Gly Arg
100 105 110

Leu Gly Gly Ile Arg Val Ala Tyr Phe Gly Leu Thr Thr Leu Ser Ala
115 120 125

Ser Ala Leu Ala Val Ala Leu Ala Phe Ile Ile Lys Pro Gly Ser Gly
130 135 140

Ala Gln Thr Leu Gln Ser Ser Asp Leu Gly Leu Glu Asp Ser Gly Pro
145 150 155 160

Pro Pro Val Pro Lys Glu Thr Val Asp Ser Phe Leu Asp Leu Ala Arg
165 170 175

Asn Leu Phe Pro Ser Asn Leu Val Val Ala Ala Phe Arg Thr Tyr Ala
180 185 190

Thr Asp Tyr Lys Val Val Thr Gln Asn Ser Ser Ser Gly Asn Val Thr
195 200 205

His Glu Lys Ile Pro Ile Gly Thr Glu Ile Glu Gly Met Asn Ile Leu
210 215 220

Gly Leu Val Leu Phe Ala Leu Val Leu Gly Val Ala Leu Lys Lys Leu
225 230 235 240

Gly Ser Glu Gly Glu Asp Leu Ile Arg Phe Phe Asn Ser Leu Asn Glu
245 250 255

Ala Thr Met Val Leu Val Ser Trp Ile Met Trp Tyr Val Pro Val Gly
260 265 270

Ile Met Phe Leu Val Gly Ser Lys Ile Val Glu Met Lys Asp Ile Ile
275 280 285

Val Leu Val Thr Ser Leu Gly Lys Tyr Ile Phe Ala Ser Ile Leu Gly
290 295 300

His Val Ile His Gly Gly Ile Val Leu Pro Leu Ile Tyr Phe Val Phe
305 310 315 320

Thr Arg Lys Asn Pro Phe Arg Phe Leu Leu Gly Leu Leu Ala Pro Phe
325 330 335

Ala Thr Ala Phe Ala Thr Cys Ser Ser Ser Ala Thr Leu Pro Ser Met
340 345 350

Met	Lys	Cys	Ile	Glu	Glu	Asn	Asn	Gly	Val	Asp	Lys	Arg	Ile	Ser	Arg
355						360					365				
Phe	Ile	Leu	Pro	Ile	Gly	Ala	Thr	Val	Asn	Met	Asp	Gly	Ala	Ala	Ile
370						375					380				
Phe	Gln	Cys	Val	Ala	Ala	Val	Phe	Ile	Ala	Gln	Leu	Asn	Asn	Ile	Glu
385						390				395					400
Leu	Asn	Ala	Gly	Gln	Ile	Phe	Thr	Ile	Leu	Val	Thr	Ala	Thr	Ala	Ser
						405			410					415	
Ser	Val	Gly	Ala	Ala	Gly	Val	Pro	Ala	Gly	Gly	Val	Leu	Thr	Ile	Ala
						420			425					430	
Ile	Ile	Leu	Glu	Ala	Ile	Gly	Leu	Pro	Thr	His	Asp	Leu	Pro	Leu	Ile
						435			440					445	
Leu	Ala	Val	Asp	Trp	Ile	Val	Asp	Arg	Thr	Thr	Thr	Val	Val	Asn	Val
						450			455					460	
Glu	Gly	Asp	Ala	Leu	Gly	Ala	Gly	Ile	Leu	His	His	Leu	Asn	Gln	Lys
465						470			475					480	
Ala	Thr	Lys	Lys	Gly	Glu	Gln	Glu	Leu	Ala	Glu	Val	Lys	Val	Glu	Ala
						485			490					495	
Ile	Pro	Asn	Cys	Lys	Ser	Glu	Glu	Glu	Thr	Ser	Pro	Leu	Val	Thr	His
						500			505					510	
Gln	Asn	Pro	Ala	Gly	Pro	Val	Ala	Ser	Ala	Pro	Glu	Leu	Glu	Ser	Lys
						515			520					525	
Glu	Ser	Val	Leu												
						530									

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: 5'UTR
 - (B) LOCATION: 1..30
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 31..1656
- (ix) FEATURE:
 - (A) NAME/KEY: 3'UTR
 - (B) LOCATION: 1657..1680
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGAAGAGA CCCTCCTAGA AAAGTAAAAT ATG ACT AAA AGC AAT GGA GAA GAG Met Thr Lys Ser Asn Gly Glu Glu 1 5	54
CCC AAG ATG GGG GGC AGG ATG GAG AGA TTC CAG CAG GGA GTC CGT AAA Pro Lys Met Gly Gly Arg Met Glu Arg Phe Gln Gln Gly Val Arg Lys 10 15 20	102
CGC ACA CTT TTG GCC AAG AAG AAA GTG CAG AAC ATT ACA AAG GAG GTT Arg Thr Leu Leu Ala Lys Lys Val Gln Asn Ile Thr Lys Glu Val 25 30 35 40	150
GTT AAA AGT TAC CTG TTT CGG AAT GCT TTT GTG CTG CTC ACA GTC ACC Val Lys Ser Tyr Leu Phe Arg Asn Ala Phe Val Leu Leu Thr Val Thr 45 50 55	198
GCT GTC ATT GTG GGT ACA ATC CTT GGA TTT ACC CTC CGA CCA TAC AGA Ala Val Ile Val Gly Thr Ile Leu Gly Phe Thr Leu Arg Pro Tyr Arg 60 65 70	246
ATG AGC TAC CGG GAA GTC AAG TAC TTC TCC TTT CCT GGG GAA CTT CTG Met Ser Tyr Arg Glu Val Lys Tyr Phe Ser Phe Pro Gly Glu Leu Leu 75 80 85	294
ATG AGG ATG TTA CAG ATG CTG GTC TTA CCA CTT ATC ATC TCC AGT CTT Met Arg Met Leu Gln Met Leu Val Pro Leu Ile Ile Ser Ser Leu 90 95 100	342
GTC ACA GGA ATG GCG GCG CTA GAT AGT AAG GCA TCA GGG AAG TGG GAA Val Thr Gly Met Ala Ala Leu Asp Ser Lys Ala Ser Gly Lys Trp Glu 105 110 115 120	390
TGC GGA GCT GTA GTC TAT TAT ATG ACT ACC ACC ATC ATT GCT GTG GTG Cys Gly Ala Val Val Tyr Tyr Met Thr Thr Ile Ile Ala Val Val 125 130 135	438
ATT GGC ATA ATC ATT GTC ATC ATC ATC CAT CCT GGG AAG GGC ACA AAG Ile Gly Ile Ile Val Ile Ile His Pro Gly Lys Gly Thr Lys 140 145 150	486
GAA AAC ATG CAC AGA GAA GGC AAA ATT GTA CGA GTG ACA GCT GCA GAT Glu Asn Met His Arg Glu Gly Lys Ile Val Arg Val Thr Ala Ala Asp 155 160 165	534
GCC TTC CTG GAC TTG ATC AGG AAC ATG TTA AAT CCA AAT CTG GTA GAA Ala Phe Leu Asp Leu Ile Arg Asn Met Leu Asn Pro Asn Leu Val Glu 170 175 180	582
GCC TGC TTT AAA CAG TTT AAA ACC AAC TAT GAG AAG AGA AGC TTT AAA Ala Cys Phe Lys Gln Phe Lys Thr Asn Tyr Glu Lys Arg Ser Phe Lys 185 190 195 200	630
GTG CCC ATC CAG GCC AAC GAA ACG CTT GTG GGT GCT GTG ATA AAC AAT Val Pro Ile Gln Ala Asn Glu Thr Leu Val Gly Ala Val Ile Asn Asn 205 210 215	678
GTG TCT GAG GCC ATG GAG ACT CTT ACC CGA ATC ACA GAG GAG CTG GTC Val Ser Glu Ala Met Glu Thr Leu Thr Arg Ile Thr Glu Glu Leu Val 220 225 230	726

CCA GTT CCA GGA TCT GTG AAT GGA GTC AAT GCC CTG GGT CTA GTT GTC	774
Pro Val Pro Gly Ser Val Asn Gly Val Asn Ala Leu Gly Leu Val Val	
235 240 245	
TTC TCC ATG TGC TTC GGT TTT GTG ATT GGA AAC ATG AAG GAA CAG GGG	822
Phe Ser Met Cys Phe Gly Phe Val Ile Gly Asn Met Lys Glu Gln Gly	
250 255 260	
CAG GCC CTG AGA GAG TTC TTT GAT TCT CTT AAC GAA GCC ATC ATG AGA	870
Gln Ala Leu Arg Glu Phe Phe Asp Ser Leu Asn Glu Ala Ile Met Arg	
265 270 275 280	
CTG GTA GCA GTA ATA ATG TGG TAT GCC CCC GTG GGT ATT CTC TTC CTG	918
Leu Val Ala Val Ile Met Trp Tyr Ala Pro Val Gly Ile Leu Phe Leu	
285 290 295	
ATT GCT GGG AAG ATT GTG GAG ATG GAA GAC ATG GGT GTG ATT GGG GGG	966
Ile Ala Gly Lys Ile Val Glu Met Glu Asp Met Gly Val Ile Gly Gly	
300 305 310	
CAG CTT GCC ATG TAC ACC GTG ACT GTC ATT GTT GGC TTA CTC ATT CAC	1014
Gln Leu Ala Met Tyr Thr Val Thr Val Ile Val Gly Leu Leu Ile His	
315 320 325	
GCA GTC ATC GTC TTG CCA CTC CTC TAC TTC TTG GTA ACA CGG AAA AAC	1062
Ala Val Ile Val Leu Pro Leu Leu Tyr Phe Leu Val Thr Arg Lys Asn	
330 335 340	
CCT TGG GTT TTT ATT GGA GGG TTG CTG CAA GCA CTC ATC ACC GCT CTG	1110
Pro Trp Val Phe Ile Gly Gly Leu Leu Gln Ala Leu Ile Thr Ala Leu	
345 350 355 360	
GGG ACC TCT TCA AGT TCT GCC ACC CTA CCC ATC ACC TTC AAG TGC CTG	1158
Gly Thr Ser Ser Ser Ala Thr Leu Pro Ile Thr Phe Lys Cys Leu	
365 370 375	
GAA GAG AAC AAT GGC GTG GAC AAG CGC GTC ACC AGA TTC GTG CTC CCC	1206
Glu Glu Asn Asn Gly Val Asp Lys Arg Val Thr Arg Phe Val Leu Pro	
380 385 390	
GTA GGA GCC ACC ATT AAC ATG GAT GGG ACT GCC CTC TAT GAG GCT TTG	1254
Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Leu	
395 400 405	
GCT GCC ATT TTC ATT GCT CAA GTT AAC AAC TTT GAA CTG AAC TTC GGA	1302
Ala Ala Ile Phe Ile Ala Gln Val Asn Asn Phe Glu Leu Asn Phe Gly	
410 415 420	
CAA ATT ATT ACA ATC AGC ATC ACA GCC ACA GCT GCC AGT ATT GGG GCA	1350
Gln Ile Ile Thr Ile Ser Ile Thr Ala Thr Ala Ala Ser Ile Gly Ala	
425 430 435 440	
GCT GGA ATT CCT CAG GCG GGC CTG GTC ACT ATG GTC ATT GTG CTG ACA	1398
Ala Gly Ile Pro Gln Ala Gly Leu Val Thr Met Val Ile Val Leu Thr	
445 450 455	
TCT GTC GGC CTG CCC ACT GAC GAC ATC ACG CTC ATC ATC GCG GTG GAC	1446
Ser Val Gly Leu Pro Thr Asp Asp Ile Thr Leu Ile Ile Ala Val Asp	
460 465 470	

TGG TTC TTG GAT CGC CTC CGG ACC ACC ACC AAC GTA CTG GGA GAC TCC	1494
Trp Phe Leu Asp Arg Leu Arg Thr Thr Thr Asn Val Leu Gly Asp Ser	
475 480 485	
CTG GGA GCT GGG ATT GTG GAG CAC TTG TCA CGA CAT GAA CTG AAG AAC	1542
Leu Gly Ala Gly Ile Val Glu His Leu Ser Arg His Glu Leu Lys Asn	
490 495 500	
AGA GAT GTT GAA ATG GGT AAC TCA GTG ATT GAA GAG AAT GAA ATG AAG	1590
Arg Asp Val Glu Met Gly Asn Ser Val Ile Glu Glu Asn Glu Met Lys	
505 510 515 520	
AAA CCA TAT CAA CTG ATT GCA CAG GAC AAT GAA ACT GAG AAA CCC ATC	1638
Lys Pro Tyr Gln Leu Ile Ala Gln Asp Asn Glu Thr Glu Lys Pro Ile	
525 530 535	
GAC AGT GAA ACC AAG ATG TAGACTAACCA TAAAGAAACA CTTT	1680
Asp Ser Glu Thr Lys Met	
540	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Thr Lys Ser Asn Gly Glu Glu Pro Lys Met Gly Gly Arg Met Glu
 1 5 10 15

Arg Phe Gln Gln Gly Val Arg Lys Arg Thr Leu Leu Ala Lys Lys Lys
 20 25 30

Val Gln Asn Ile Thr Lys Glu Val Val Lys Ser Tyr Leu Phe Arg Asn
 35 40 45

Ala Phe Val Leu Leu Thr Val Thr Ala Val Ile Val Gly Thr Ile Leu
 50 55 60

Gly Phe Thr Leu Arg Pro Tyr Arg Met Ser Tyr Arg Glu Val Lys Tyr
 65 70 75 80

Phe Ser Phe Pro Gly Glu Leu Leu Met Arg Met Leu Gln Met Leu Val
 85 90 95

Leu Pro Leu Ile Ile Ser Ser Leu Val Thr Gly Met Ala Ala Leu Asp
 100 105 110

Ser Lys Ala Ser Gly Lys Trp Glu Cys Gly Ala Val Val Tyr Tyr Met
 115 120 125

Thr Thr Thr Ile Ile Ala Val Val Ile Gly Ile Ile Ile Val Ile Ile
 130 135 140

Ile His Pro Gly Lys Gly Thr Lys Glu Asn Met His Arg Glu Gly Lys
145 150 155 160

Ile Val Arg Val Thr Ala Ala Asp Ala Phe Leu Asp Leu Ile Arg Asn
165 170 175

Met Leu Asn Pro Asn Leu Val Glu Ala Cys Phe Lys Gln Phe Lys Thr
180 185 190

Asn Tyr Glu Lys Arg Ser Phe Lys Val Pro Ile Gln Ala Asn Glu Thr
195 200 205

Leu Val Gly Ala Val Ile Asn Asn Val Ser Glu Ala Met Glu Thr Leu
210 215 220

Thr Arg Ile Thr Glu Glu Leu Val Pro Val Pro Gly Ser Val Asn Gly
225 230 235 240

Val Asn Ala Leu Gly Leu Val Val Phe Ser Met Cys Phe Gly Phe Val
245 250 255

Ile Gly Asn Met Lys Glu Gln Gly Gln Ala Leu Arg Glu Phe Phe Asp
260 265 270

Ser Leu Asn Glu Ala Ile Met Arg Leu Val Ala Val Ile Met Trp Tyr
275 280 285

Ala Pro Val Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Val Glu Met
290 295 300

Glu Asp Met Gly Val Ile Gly Gly Gln Leu Ala Met Tyr Thr Val Thr
305 310 315 320

Val Ile Val Gly Leu Leu Ile His Ala Val Ile Val Leu Pro Leu Leu
325 330 335

Tyr Phe Leu Val Thr Arg Lys Asn Pro Trp Val Phe Ile Gly Gly Leu
340 345 350

Leu Gln Ala Leu Ile Thr Ala Leu Gly Thr Ser Ser Ser Ala Thr
355 360 365

Leu Pro Ile Thr Phe Lys Cys Leu Glu Glu Asn Asn Gly Val Asp Lys
370 375 380

Arg Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp
385 390 395 400

Gly Thr Ala Leu Tyr Glu Ala Leu Ala Ala Ile Phe Ile Ala Gln Val
405 410 415

Asn Asn Phe Glu Leu Asn Phe Gly Gln Ile Ile Thr Ile Ser Ile Thr
420 425 430

Ala Thr Ala Ala Ser Ile Gly Ala Ala Gly Ile Pro Gln Ala Gly Leu
435 440 445

Val Thr Met Val Ile Val Leu Thr Ser Val Gly Leu Pro Thr Asp Asp
450 455 460

Ilé	Thr	Leu	Ile	Ile	Ala	Val	Asp	Trp	Phe	Leu	Asp	Arg	Leu	Arg	Thr
465					470					475					480
Thr	Thr	Asn	Val	Leu	Gly	Asp	Ser	Leu	Gly	Ala	Gly	Ile	Val	Glu	His
					485				490					495	
Leu	Ser	Arg	His	Glu	Leu	Lys	Asn	Arg	Asp	Val	Glu	Met	Gly	Asn	Ser
				500				505					510		
Val	Ile	Glu	Glu	Asn	Glu	Met	Lys	Lys	Pro	Tyr	Gln	Leu	Ile	Ala	Gln
		515				520						525			
Asp	Asn	Glu	Thr	Glu	Lys	Pro	Ile	Asp	Ser	Glu	Thr	Lys	Met		
		530				535					540				

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1800 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: 5'UTR
 - (B) LOCATION: 1..33
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 34..1755
- (ix) FEATURE:
 - (A) NAME/KEY: 3'UTR
 - (B) LOCATION: 1756..1800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATAGTGCTG AAGAGGAGGG GCGTTCCCAG ACC ATG GCA TCT ACG GAA GGT GCC	54
Met Ala Ser Thr Glu Gly Ala	
1 5	
AAC AAT ATG CCC AAG CAG GTG GAA GTG CGA ATG CCA GAC AGT CAT CTT	102
Asn Asn Met Pro Lys Gln Val Glu Val Arg Met Pro Asp Ser His Leu	
10 15 20	
GGC TCA GAG GAA CCC AAG CAC CGG CAC CTG GGC CTG CGC CTG TGT GAC	150
Gly Ser Glu Glu Pro Lys His Arg His Leu Gly Leu Arg Leu Cys Asp	
25 30 35	
AAG CTG GGG AAG AAT CTG CTG CTC ACC CTG ACG GTG TTT GGT GTC ATC	198
Lys Leu Gly Lys Asn Leu Leu Leu Thr Leu Thr Val Phe Gly Val Ile	
40 45 50 55	
CTG GGA GCA GTG TGT GGA GGG CTT CTT CGC TTG GCA TCT CCC ATC CAC	246
Leu Gly Ala Val Cys Gly Gly Leu Leu Arg Leu Ala Ser Pro Ile His	
60 65 70	

CCT GAT GTG GTT ATG TTA ATA GCC TTC CCA GGG GAT ATA CTC ATG AGG	294
Pro Asp Val Val Met Leu Ile Ala Phe Pro Gly Asp Ile Leu Met Arg	
75 80 85	
ATG CTA AAA ATG CTC ATT CTG GGT CTA ATC ATC TCC AGC TTA ATC ACA	342
Met Leu Lys Met Leu Ile Leu Gly Leu Ile Ile Ser Ser Leu Ile Thr	
90 95 100	
GGG TTG TCA GGC CTG GAT GCT AAG GCT AGT GGC CGC TTG GGC ACG AGA	390
Gly Leu Ser Gly Leu Asp Ala Lys Ala Ser Gly Arg Leu Gly Thr Arg	
105 110 115	
GCC ATG GTG TAT TAC ATG TCC ACG ACC ATC ATT GCT GCA GTA CTG GGG	438
Ala Met Val Tyr Tyr Met Ser Thr Thr Ile Ile Ala Ala Val Leu Gly	
120 125 130 135	
GTC ATT CTG GTC TTG GCT ATC CAT CCA GGC AAT CCC AAG CTC AAG AAG	486
Val Ile Leu Val Leu Ala Ile His Pro Gly Asn Pro Lys Leu Lys Lys	
140 145 150	
CAG CTG GGG CCT GGG AAG AAG AAT GAT GAA GTG TCC AGC CTG GAT GCC	534
Gln Leu Gly Pro Gly Lys Lys Asn Asp Glu Val Ser Ser Leu Asp Ala	
155 160 165	
TTC CTG GAC CTT ATT CGA AAT CTC TTC CCT GAA AAC CTT GTC CAA GCC	582
Phe Leu Asp Leu Ile Arg Asn Leu Phe Pro Glu Asn Leu Val Gln Ala	
170 175 180	
TGC TTT CAA CAG ATT CAA ACA GTG ACG AAG AAA GTC CTG GTT GCA CCA	630
Cys Phe Gln Gln Ile Gln Thr Val Thr Lys Lys Val Leu Val Ala Pro	
185 190 195	
CCG CCA GAC GAG GAG GCC AAC GCA ACC AGC GCT GAA GTC TCT CTG TTG	678
Pro Pro Asp Glu Glu Ala Asn Ala Thr Ser Ala Glu Val Ser Leu Leu	
200 205 210 215	
AAC GAG ACT GTG ACT GAG GTG CCG GAG GAG ACT AAG ATG GTT ATC AAG	726
Asn Glu Thr Val Thr Glu Val Pro Glu Glu Thr Lys Met Val Ile Lys	
220 225 230	
AAG GGC CTG GAG TTC AAG GAT GGG ATG AAC GTC TTA GGT CTG ATA GGG	774
Lys Gly Leu Glu Phe Lys Asp Gly Met Asn Val Leu Gly Leu Ile Gly	
235 240 245	
TTT TTC ATT GCT TTT GGC ATC GCT ATG GGG AAG ATG GGA GAT CAG GCC	822
Phe Phe Ile Ala Phe Gly Ile Ala Met Gly Lys Met Gly Asp Gln Ala	
250 255 260	
AAG CTG ATG GTG GAT TTC TTC AAC ATT TTG AAT GAG ATT GTA ATG AAG	870
Lys Leu Met Val Asp Phe Phe Asn Ile Leu Asn Glu Ile Val Met Lys	
265 270 275	
TTA GTG ATC ATG ATC ATG TGG TAC TCT CCC CTG GGT ATC GCC TGC CTG	918
Leu Val Ile Met Ile Met Trp Tyr Ser Pro Leu Gly Ile Ala Cys Leu	
280 285 290 295	
ATC TGT GGA AAG ATC ATT GCA ATC AAG GAC TTA GAA GTG GTT GCT AGG	966
Ile Cys Gly Lys Ile Ile Ala Ile Lys Asp Leu Glu Val Val Ala Arg	
300 305 310	

CAA CTG GGG ATG TAC ATG GTA ACA GTG ATC ATA GGC CTC ATC ATC CAC		1014
Gln Leu Gly Met Tyr Met Val Thr Val Ile Ile Gly Leu Ile Ile His		
315 320 325		
GGG GGC ATC TTT CTC CCC TTG ATT TAC TTT GTA GTG ACC AGG AAA AAC		1062
Gly Gly Ile Phe Leu Pro Leu Ile Tyr Phe Val Val Thr Arg Lys Asn		
330 335 340		
CCC TTC TCC CTT TTT GCT GGC ATT TTC CAA GCT TGG ATC ACT GCC CTG		1110
Pro Phe Ser Leu Phe Ala Gly Ile Phe Gln Ala Trp Ile Thr Ala Leu		
345 350 355		
GGC ACC GCT TCC AGT GCT GGA ACT TTG CCT GTC ACC TTT CGT TGC CTG		1158
Gly Thr Ala Ser Ser Ala Gly Thr Leu Pro Val Thr Phe Arg Cys Leu		
360 365 370 375		
GAA GAA AAT CTG GGG ATT GAT AAG CGT GTG ACT AGA TTC GTC CTT CCT		1206
Glu Glu Asn Leu Gly Ile Asp Lys Arg Val Thr Arg Phe Val Leu Pro		
380 385 390		
GTT GGA GCA ACC ATT AAC ATG GAT GGT ACA GCC CTT TAT GAA GCG GTG		1254
Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val		
395 400 405		
GCC GCC ATC TTT ATA GCC CAA ATG AAT GGT GTT GTC CTG GAT GGA GGA		1302
Ala Ala Ile Phe Ile Ala Gln Met Asn Gly Val Val Leu Asp Gly Gly		
410 415 420		
CAG ATT GTG ACT GTA AGC CTC ACA GCC ACC CTG GCA AGC GTC GGC GCG		1350
Gln Ile Val Thr Val Ser Leu Thr Ala Thr Leu Ala Ser Val Gly Ala		
425 430 435		
GCC AGT ATC CCC AGT GCC GGG CTG GTC ACC ATG CTC CTC ATT CTG ACA		1398
Ala Ser Ile Pro Ser Ala Gly Leu Val Thr Met Leu Leu Ile Leu Thr		
440 445 450 455		
GCC GTG GGC CTG CCA ACA GAG GAC ATC AGC TTG CTG GTG GCT GTG GAC		1446
Ala Val Gly Leu Pro Thr Glu Asp Ile Ser Leu Leu Val Ala Val Asp		
460 465 470		
TGG CTG CTG GAC AGG ATG AGA ACT TCA GTC AAT GTT GTG GGT GAC TCT		1494
Trp Leu Leu Asp Arg Met Arg Thr Ser Val Asn Val Val Gly Asp Ser		
475 480 485		
TTT GGG GCT GGG ATA GTC TAT CAC CTC TCC AAG TCT GAG CTG GAT ACC		1542
Phe Gly Ala Gly Ile Val Tyr His Leu Ser Lys Ser Glu Leu Asp Thr		
490 495 500		
ATT GAC TCC CAG CAT CGA GTG CAT GAA GAT ATT GAA ATG ACC AAG ACT		1590
Ile Asp Ser Gln His Arg Val His Glu Asp Ile Glu Met Thr Lys Thr		
505 510 515		
CAA TCC ATT TAT GAT GAC ATG AAG AAC CAC AGG GAA AGC AAC TCT AAT		1638
Gln Ser Ile Tyr Asp Asp Met Lys Asn His Arg Glu Ser Asn Ser Asn		
520 525 530 535		
CAA TGT GTC TAT GCT GCA CAC AAC TCT GTC ATA GTA GAT GAA TGC AAG		1686
Gln Cys Val Tyr Ala Ala His Asn Ser Val Ile Val Asp Glu Cys Lys		
540 545 550		

GTA ACT CTG GCA GCC AAT GGA AAG TCA GCC GAC TGC AGT GTT GAG GAA	1734
Val Thr Leu Ala Ala Asn Gly Lys Ser Ala Asp Cys Ser Val Glu Glu	
555	560
565	
GAA CCT TGG AAA CGT GAG AAA TAAGGATATG AGTCTCAGCA AATTCTTGAA	1785
Glu Pro Trp Lys Arg Glu Lys	
570	
TAAACTCCCC AGCGT	1800

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Thr Glu Gly Ala Asn Asn Met Pro Lys Gln Val Glu Val
 1 5 10 15

Arg Met Pro Asp Ser His Leu Gly Ser Glu Glu Pro Lys His Arg His
 20 25 30

Leu Gly Leu Arg Leu Cys Asp Lys Leu Gly Lys Asn Leu Leu Thr
 35 40 45

Leu Thr Val Phe Gly Val Ile Leu Gly Ala Val Cys Gly Gly Leu Leu
 50 55 60

Arg Leu Ala Ser Pro Ile His Pro Asp Val Val Met Leu Ile Ala Phe
 65 70 75 80

Pro Gly Asp Ile Leu Met Arg Met Leu Lys Met Leu Ile Leu Gly Leu
 85 90 95

Ile Ile Ser Ser Leu Ile Thr Gly Leu Ser Gly Leu Asp Ala Lys Ala
 100 105 110

Ser Gly Arg Leu Gly Thr Arg Ala Met Val Tyr Tyr Met Ser Thr Thr
 115 120 125

Ile Ile Ala Ala Val Leu Gly Val Ile Leu Val Leu Ala Ile His Pro
 130 135 140

Gly Asn Pro Lys Leu Lys Lys Gln Leu Gly Pro Gly Lys Lys Asn Asp
 145 150 155 160

Glu Val Ser Ser Leu Asp Ala Phe Leu Asp Leu Ile Arg Asn Leu Phe
 165 170 175

Pro Glu Asn Leu Val Gln Ala Cys Phe Gln Gln Ile Gln Thr Val Thr
 180 185 190

Lys Lys Val Leu Val Ala Pro Pro Pro Asp Glu Glu Ala Asn Ala Thr

195

200

205

Ser Ala Glu Val Ser Leu Leu Asn Glu Thr Val Thr Glu Val Pro Glu
210 215 220

Glu Thr Lys Met Val Ile Lys Lys Gly Leu Glu Phe Lys Asp Gly Met
225 230 235 240

Asn Val Leu Gly Leu Ile Gly Phe Phe Ile Ala Phe Gly Ile Ala Met
245 250 255

Gly Lys Met Gly Asp Gln Ala Lys Leu Met Val Asp Phe Phe Asn Ile
260 265 270

Leu Asn Glu Ile Val Met Lys Leu Val Ile Met Ile Met Trp Tyr Ser
275 280 285

Pro Leu Gly Ile Ala Cys Leu Ile Cys Gly Lys Ile Ile Ala Ile Lys
290 295 300

Asp Leu Glu Val Val Ala Arg Gln Leu Gly Met Tyr Met Val Thr Val
305 310 315 320

Ile Ile Gly Leu Ile Ile His Gly Gly Ile Phe Leu Pro Leu Ile Tyr
325 330 335

Phe Val Val Thr Arg Lys Asn Pro Phe Ser Leu Phe Ala Gly Ile Phe
340 345 350

Gln Ala Trp Ile Thr Ala Leu Gly Thr Ala Ser Ser Ala Gly Thr Leu
355 360 365

Pro Val Thr Phe Arg Cys Leu Glu Glu Asn Leu Gly Ile Asp Lys Arg
370 375 380

Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp Gly
385 390 395 400

Thr Ala Leu Tyr Glu Ala Val Ala Ala Ile Phe Ile Ala Gln Met Asn
405 410 415

Gly Val Val Leu Asp Gly Gly Gln Ile Val Thr Val Ser Leu Thr Ala
420 425 430

Thr Leu Ala Ser Val Gly Ala Ala Ser Ile Pro Ser Ala Gly Leu Val
435 440 445

Thr Met Leu Leu Ile Leu Thr Ala Val Gly Leu Pro Thr Glu Asp Ile
450 455 460

Ser Leu Leu Val Ala Val Asp Trp Leu Leu Asp Arg Met Arg Thr Ser
465 470 475 480

Val Asn Val Val Gly Asp Ser Phe Gly Ala Gly Ile Val Tyr His Leu
485 490 495

Ser Lys Ser Glu Leu Asp Thr Ile Asp Ser Gln His Arg Val His Glu
500 505 510

Asp	Ile	Glu	Met	Thr	Lys	Thr	Gln	Ser	Ile	Tyr	Asp	Asp	Met	Lys	Asn
515							520						525		
His	Arg	Glu	Ser	Asn	Ser	Asn	Gln	Cys	Val	Tyr	Ala	Ala	His	Asn	Ser
530							535						540		
Val	Ile	Val	Asp	Glu	Cys	Lys	Val	Thr	Leu	Ala	Ala	Asn	Gly	Lys	Ser
545							550						555		560
Ala	Asp	Cys	Ser	Val	Glu	Glu	Pro	Trp	Lys	Arg	Glu	Lys			
				565				570							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..1590

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1591..1674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATAGCGGCCGA	CAGCC	ATG	GGG	AAA	CCG	GCG	AGG	AAA	GGA	TGC	CCG	AGT	TGG		51		
		Met	Gly	Lys	Pro	Ala	Arg	Lys	Gly	Cys	Pro	Ser	Trp				
1													10				
AAG	CGC	TTC	CTG	AAG	AAT	AAC	TGG	GTG	TTG	CTG	TCC	ACC	GTG	GCC	GCG	99	
		Lys	Arg	Phe	Leu	Lys	Asn	Asn	Trp	Val	Leu	Leu	Ser	Thr	Val	Ala	Ala
15													25				
GTG	GTG	CTA	GGC	ATT	ACC	ACA	GGA	GTC	TTG	GTT	CGA	GAA	CAC	AGC	AAC	147	
		Val	Val	Leu	Gly	Ile	Thr	Thr	Gly	Val	Leu	Val	Arg	Glu	His	Ser	Asn
30													40				
CTC	TCA	ACT	CTA	GAG	AAA	TTC	TAC	TTT	GCT	TTT	CCT	GGA	GAA	ATT	CTA	195	
		Leu	Ser	Thr	Leu	Glu	Lys	Phe	Tyr	Phe	Ala	Phe	Pro	Gly	Glu	Ile	Leu
45													55		60		
ATG	CGG	ATG	CTG	AAA	CTC	ATC	ATT	TTG	CCA	TTA	ATT	ATA	TCC	AGC	ATG	243	
		Met	Arg	Met	Leu	Lys	Leu	Ile	Ile	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Met
65													75				
ATT	ACA	GGT	GTT	GCT	GCA	CTG	GAT	TCC	AAC	GTA	TCC	GGA	AAA	ATT	GGT	291	
		Ile	Thr	Gly	Val	Ala	Ala	Leu	Asp	Ser	Asn	Val	Ser	Gly	Lys	Ile	Gly
80													85		90		

CTG CGC GCT GTC GTG TAT TAT TTC TGT ACC ACT CTC ATT GCT GTT ATT	339
Leu Arg Ala Val Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile	
95 100 105	
CTA GGT ATT GTG CTG GTG AGC ATC AAG CCT GGT GTC ACC CAG AAA	387
Leu Gly Ile Val Leu Val Ser Ile Lys Pro Gly Val Thr Gln Lys	
110 115 120	
GTG GGT GAA ATT GCG AGG ACA GGC AGC ACC CCT GAA GTC AGT ACG GTG	435
Val Gly Glu Ile Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val	
125 130 135 140	
GAT GCC ATG TTA GAT CTC ATC AGG AAT ATG TTC CCT GAG AAT CTT GTC	483
Asp Ala Met Leu Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val	
145 150 155	
CAG GCC TGT TTT CAG CAG TAC AAA ACT AAG CGT GAA GAA GTG AAG CCT	531
Gln Ala Cys Phe Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro	
160 165 170	
CCC AGC GAT CCA GAG ATG AAC ATG ACA GAA GAG TCC TTC ACA GCT GTC	579
Pro Ser Asp Pro Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val	
175 180 185	
ATG ACA ACT GCA ATT TCC AAG AAC AAA ACA AAG GAA TAC AAA ATT GTT	627
Met Thr Thr Ala Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val	
190 195 200	
GGC ATG TAT TCA GAT GGC ATA AAC GTC CTG GGC TTG ATT GTC TTT TGC	675
Gly Met Tyr Ser Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys	
205 210 215 220	
CTT GTC TTT GGA CTT GTC ATT GGA AAA ATG GGA GAA AAG GGA CAA ATT	723
Leu Val Phe Gly Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile	
225 230 235	
CTG GTG GAT TTC TTC AAT GCT TTG AGT GAT GCA ACC ATG AAA ATC GTT	771
Leu Val Asp Phe Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val	
240 245 250	
CAG ATC ATC ATG TGT TAT ATG CCA CTA GGT ATT TTG TTC CTG ATT GCT	819
Gln Ile Ile Met Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala	
255 260 265	
GGG AAG ATC ATA GAA GTT GAA GAC TGG GAA ATA TTC CGC AAG CTG GGC	867
Gly Lys Ile Ile Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly	
270 275 280	
CTT TAC ATG GCC ACA GTC CTG ACT GGG CTT GCA ATC CAC TCC ATT GTA	915
Leu Tyr Met Ala Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val	
285 290 295 300	
ATT CTC CCG CTG ATA TAT TTC ATA GTC GTA CGA AAG AAC CCT TTC CGA	963
Ile Leu Pro Leu Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg	
305 310 315	
TTT GCC ATG GGA ATG GCC CAG GCT CTC CTG ACA GCT CTC ATG ATC TCT	1011
Phe Ala Met Gly Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser	
320 325 330	

TCC	AGT	TCA	GCA	ACA	CTG	CCT	GTC	ACC	TTC	CGC	TGT	GCT	GAA	GAA	AAT	1059
Ser	Ser	Ser	Ala	Thr	Leu	Pro	Val	Thr	Phe	Arg	Cys	Ala	Glu	Glu	Asn	
335					340							345				
AAC	CAG	GTG	GAC	AAG	AGG	ATC	ACT	CGA	TTC	GTG	TTA	CCC	GTT	GGT	GCA	1107
Asn	Gln	Val	Asp	Lys	Arg	Ile	Thr	Arg	Phe	Val	Leu	Pro	Val	Gly	Ala	
350					355						360					
ACA	ATC	AAC	ATG	GAT	GGG	ACC	GCG	CTC	TAT	GAA	GCA	GTG	GCA	GCG	GTG	1155
Thr	Ile	Asn	Met	Asp	Gly	Thr	Ala	Leu	Tyr	Glu	Ala	Val	Ala	Ala	Val	
365					370					375			380			
TTT	ATT	GCA	CAG	TTG	AAT	GAC	CTG	GAC	TTG	GGC	ATT	GGG	CAG	ATC	ATC	1203
Phe	Ile	Ala	Gln	Leu	Asn	Asp	Leu	Asp	Leu	Gly	Ile	Gly	Gln	Ile	Ile	
385					390					395						
ACC	ATC	AGT	ATC	ACG	GCC	ACA	TCT	GCC	AGC	ATC	GGA	GCT	GCT	GGC	GTG	1251
Thr	Ile	Ser	Ile	Thr	Ala	Thr	Ser	Ala	Ser	Ile	Gly	Ala	Ala	Gly	Val	
400					405					410						
CCC	CAG	GCT	GGC	CTG	GTG	ACC	ATG	GTG	ATT	GTG	CTG	AGT	GCC	GTG	GGC	1299
Pro	Gln	Ala	Gly	Leu	Val	Thr	Met	Val	Ile	Val	Leu	Ser	Ala	Val	Gly	
415					420					425						
CTG	CCC	GCC	GAG	GAT	GTC	ACC	CTG	ATC	ATT	GCT	GTC	GAC	TGG	CTC	CTG	1347
Leu	Pro	Ala	Glu	Asp	Val	Thr	Leu	Ile	Ile	Ala	Val	Asp	Trp	Leu	Leu	
430					435					440						
GAC	CGG	TTC	AGG	ACC	ATG	GTC	AAC	GTC	CTT	GGT	GAT	GCT	TTT	GGG	ACG	1395
Asp	Arg	Phe	Arg	Thr	Met	Val	Asn	Val	Leu	Gly	Asp	Ala	Phe	Gly	Thr	
445					450					455			460			
GGC	ATT	GTG	GAA	AAG	CTC	TCC	AAG	AAG	GAG	CTG	GAG	CAG	ATG	GAT	GTT	1443
Gly	Ile	Val	Glu	Lys	Leu	Ser	Lys	Lys	Glu	Leu	Glu	Gln	Met	Asp	Val	
465					470					475						
TCA	TCT	GAA	GTC	AAC	ATT	GTG	AAT	CCC	TTT	GCC	TTG	GAA	TCC	ACA	ATC	1491
Ser	Ser	Glu	Val	Asn	Ile	Val	Asn	Pro	Phe	Ala	Leu	Glu	Ser	Thr	Ile	
480					485					490						
CTT	GAC	AAC	GAA	GAC	TCA	GAC	ACC	AAG	AAG	TCT	TAT	GTC	AAT	GGA	GGC	1539
Leu	Asp	Asn	Glu	Asp	Ser	Asp	Thr	Lys	Lys	Ser	Tyr	Val	Asn	Gly	Gly	
495					500					505						
TTT	GCA	GTA	GAC	AAG	TCT	GAC	ACC	ATC	TCA	TTC	ACC	CAG	ACC	TCA	CAG	1587
Phe	Ala	Val	Asp	Lys	Ser	Asp	Thr	Ile	Ser	Phe	Thr	Gln	Thr	Ser	Gln	
510					515					520						
TTC	TAGGGCCCT	GGCTGCAGAT	GA	CTGAAAC	AAGGAAGGAC	ATT	T	CGTGAG								1640
Phe																
525																
AGTCATCTCA	AACACGGCTT	AAGGAAAAGA	GAAA													1674

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 525 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp Lys Arg Phe Leu
1 5 10 15

Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala Val Val Leu Gly
20 25 30

Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn Leu Ser Thr Leu
35 40 45

Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu Met Arg Met Leu
50 55 60

Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met Ile Thr Gly Val
65 70 75 80

Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly Leu Arg Ala Val
85 90 95

Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile Leu Gly Ile Val
100 105 110

Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys Val Gly Glu Ile
115 120 125

Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val Asp Ala Met Leu
130 135 140

Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val Gln Ala Cys Phe
145 150 155 160

Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro Pro Ser Asp Pro
165 170 175

Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val Met Thr Thr Ala
180 185 190

Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val Gly Met Tyr Ser
195 200 205

Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys Leu Val Phe Gly
210 215 220

Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile Leu Val Asp Phe
225 230 235 240

Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val Gln Ile Ile Met
245 250 255

Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Ile
260 265 270

Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly Leu Tyr Met Ala

275

280

285

Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val Ile Leu Pro Leu
 290 295 300

Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg Phe Ala Met Gly
 305 310 315 320

Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser Ser Ser Ala
 325 330 335

Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn Asn Gln Val Asp
 340 345 350

Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met
 355 360 365

Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Val Phe Ile Ala Gln
 370 375 380

Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile Thr Ile Ser Ile
 385 390 395 400

Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val Pro Gln Ala Gly
 405 410 415

Leu Val Thr Met Val Ile Val Leu Ser Ala Val Gly Leu Pro Ala Glu
 420 425 430

Asp Val Thr Leu Ile Ile Ala Val Asp Trp Leu Leu Asp Arg Phe Arg
 435 440 445

Thr Met Val Asn Val Leu Gly Asp Ala Phe Gly Thr Gly Ile Val Glu
 450 455 460

Lys Leu Ser Lys Lys Glu Leu Glu Gln Met Asp Val Ser Ser Glu Val
 465 470 475 480

Asn Ile Val Asn Pro Phe Ala Leu Glu Ser Thr Ile Leu Asp Asn Glu
 485 490 495

Asp Ser Asp Thr Lys Lys Ser Tyr Val Asn Gly Gly Phe Ala Val Asp
 500 505 510

Lys Ser Asp Thr Ile Ser Phe Thr Gln Thr Ser Gln Phe
 515 520 525

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGGTACC GCCATGGAGA AGAGCAAC

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGTCTAGA TCACAGAACCC GACTCCTTG

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGGTACC AATATGACTA AAAGCAATG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGTCTAGA CTACATCTTG GTTCACTG

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGGTACC ACCATGGCAT CTACGGAAG

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGTCTAGA TTATTCTCA CGTTCCAAG

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGGTACC GCCATGGGGA AACCGGCG

28

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC CTAGAACTGT GAGGTCTG

28